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A new rupicolous species of gecko of the genus *Hemidactylus* Oken, 1817 from the Satpura Hills, Central India

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Abstract.—We here describe a new species of rupicolous gecko from the Satpura Hills of central India. The new species is a member of the *Hemidactylus brookii* complex, and can be distinguished based on the following suite of characters: moderate sized species (SVL 54.3–74.2 mm); anterior postmental width equal to first infralabial; posterior postmental width equal to second infralabial, posterior postmental not in contact with first infralabial; enlarged, keeled, tubercles, fairly regularly arranged in 15–16 longitudinal rows on dorsum; two angular series of seven precloacal femoral pores separated by diastema of eight non-pored scales; non-pored scales equal to size of pored scales; scales bordering anterior edge of pored scales half the size of pored scales; five lamellae on digit I and seven on digit IV of manus as well as pes; lamellae on digit IV and V of pes absent on basal 25% of the digit; legs long and slender; ventral aspect of tail with broad caudal scales covering ~80% of tail; two subconical post cloacal spurs, anterior spur slightly larger than posterior spur.

Key words. *Hemidactylus brookii*, complex, taxonomy, bPTP, multivariate analysis, DNA

Citation: Mirza ZA, Raju D. 2017. A new rupicolous species of gecko of the genus *Hemidactylus* Oken, 1817 from the Satpura Hills, Central India. *Amphibian & Reptile Conservation* 11(1) [General Section]: 51–71 (e137).

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Received: 27 May 2015; **Accepted:** 20 December 2016; **Published:** 24 March 2017

Introduction

The genus *Hemidactylus* Oken, is the second most speciose gekkonid genus in the world, with ~143 species distributed globally (Uetz and Hošek 2016), its diversity being concentrated in the tropics. India is home to at least 29 species (including *H. gleadowi* Murray) and this number is likely to increase with further sampling (Giri 2008; Giri and Bauer 2008; Mirza and Sanap 2014).

During an expedition that led to the discovery of *Eublepharis satpuraensis* (Mirza, Sanap, Raju, Gawai, and Ghadekar 2014), a species of *Hemidactylus* was collected from Pachmarhi town. Superficially resembling members of the *Hemidactylus brookii* complex, it could be separated from most members of the group by the presence of enlarged subcaudal plates on the tail and other morphological characters. *Hemidactylus brookii* Gray has had a complicated taxonomic history and nearly all attempts to resolve the group have thus far failed largely due to the commensal nature of the species, and inadequate sam-

pling effort in terms of specimens and collection localities, (Bauer et al. 2010a; Mahony 2011; Rösler and Glaw 2010) and a long list of synonyms that remained unaddressed until recently. Mahony (2011) made an effort to address the taxonomic status of several synonyms and his compilation serves as a vital resource for members of this group. However, a few issues remain, for example, the obscure identity of *Hemidactylus brookii* sensu stricto, with Grays specimens being the only true exemplars of the species, as pointed out by Kathriner et al. (2014). Lajmi et al. (2016) presented a comprehensive analysis of the group in India using molecular as well as morphological data. However, due to lack of material from Pakistan, the resolution of the entire species complex is incomplete. Despite the controversial taxonomic nature of members of this group, there are several distinct morphotypes within the complex (see Kathriner et al. 2014; Lajmi et al. 2016; Mahony 2009) that need to be addressed to help resolve the systematics of the entire *H. brookii* complex.

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Following the key provided by Lajmi et al. (2016), the specimens of *Hemidactylus* from Satpura Hills show affinity to members of clade 4/*H. cf. murrayi*. Multivariate analysis and molecular data support the distinctiveness of the specimens of *Hemidactylus* obtained from Satpura, which we herein describe as a new species. A molecular phylogenetic analysis based on 302 bp of cytochrome *b* gene suggests that the new species is sister to *H. treutleri* Mahony.

Material and Methods

Morphological and meristic data: Specimens in the field were captured by hand and euthanized, followed by fixation in 4% formaldehyde buffer. The specimens were later washed to remove traces of formalin, stored in 70% ethanol, and deposited in the collection of the National Centre for Biological Sciences, Bangalore, India and the Bombay Natural History Society, Mumbai, India. All measurements were taken following Giri and Bauer (2008) with Mitutoyo™ digital calipers (to the nearest

0.1 mm): snout-vent length (SVL: from tip of snout to vent), trunk length (TRL: distance from axilla to groin measured from posterior edge of forelimb insertion to anterior edge of hind limb insertion), body width (BW: maximum width of body), crus length (CL: from base of heel to knee); tail length (TL: from vent to tip of tail), tail width (TW: measured at widest point of tail); head length (HL: distance between retroarticular process of jaw and snout-tip), head width (HW: maximum width of head), head height (HH: maximum height of head, from occiput to underside of jaws), forearm length (FL: from base of palm to elbow); ear length (EL: longest dimension of ear); orbital diameter (OD: greatest diameter of orbit), nares to eye distance (NE: distance between anteriormost point of eye and nostril), snout to eye distance (SE: distance between anteriormost point of eye and tip of snout), eye to ear distance (EE: distance from anterior edge of ear opening to posterior corner of eye), internarial distance (IN: distance between nares), interorbital distance (IO: shortest distance between left and right supraciliary scale rows) [Table 1]. Morphological and mor-

Table 1. Morphometric and mensural data for *Hemidactylus chipkali* sp. nov.

Specimen number	Holotype NCBS AT107	Paratype NCBS AT108	Paratype NCBS AT109	Paratype BNHS 2427	Paratype BNHS 2426
Sex	♂	♀	♂	♀	♂
SVL	74.2	65.6	60.1	61.7	54.3
TRL	26.7	26	24.1	25.8	23.7
BW	11.7	13.9	12.0	12.5	10.4
CL	10.8	11.2	10.5	11.7	10.1
TL	59.4	60.4	37.6*	70.7	50*
TW	5.4	5.9	7.7	6.6	6
HL	13.4	16.7	18.4	17.5	17
HW	12.5	12.2	12.4	11.5	10.9
HH	6.5	5.9	7.1	5.5	5.4
FL	8.9	9.2	10.3	9.4	8.5
OD	4.0	3.5	3.2	3.3	3.6
NE	5.5	5.8	6.3	5.0	5.3
SE	7.2	7.9	7.	6.4	6.8
EE	4.4	5.0	4.9	4.8	4.3
EL	1.2	1.3	1.3	1.2	1.2
IN	1.4	1.5	1.5	1.5	1.2
IO	4.1	4.5	4.3	4.0	4.1
Lamellae L manus	5-6-7-7-6	5-7-7-7-8	5-7-7-7-7	5-7-7-7-7	5-7-7-7-7
Lamellae R manus	5-7-7-7-7	5-7-7-7-8	5-7-7-7-7	5-7-7-7-7	5-7-7-7-7
Lamellae L pes	5-7-7-7-7	5-8-8-8-7	5-7-8-7-6	5-7-8-7-7	5-7-8-7-7
Lamellae R pes	5-7-8-7-6	5-8-8-7-7	5-7-8-7-7	5-7-8-7-7	5-8-8-7-7
Supralabials Left	12	10	11	10	10
Supralabials R	11	11	11	11	10
Infralabials L	9	9	9	10	8
Infralabials R	10	9	10	9	8
Pores L/R	7/7	-	8/8	-	8/8
gap between pores	8	-	8	-	8

phometric data for *Hemidactylus brookii* group was obtained from, Lajmi et al. (2016), Mahony (2011), Rösler and Glaw (2010). Principal Component Analysis (PCA) was performed to further support the distinctiveness of the new species. Meristic counts and external observations of morphology were made using a Leica™ S8A-PO dissecting microscope. Images of the specimens were taken with a Canon™ 70D mounted with a Canon™ 100 mm macro illuminated with two external Canon™ 430EX-II flashes, and plates were edited in Adobe® Photoshop CS5 (<http://www.adobe.com/legal/permissions/trademarks.html>). Institutional acronyms used in the manuscript are as follows: BNHS (Bombay Natural History Society), Mumbai; NHM (Natural History Museum London); NCBS (Collection facility, National Centre for Biological Sciences), Bangalore; ZSI (Zoological Survey of India), Kolkata.

Molecular methods and analysis: Genomic DNA for a single specimen was extracted from tail tissue using the Phenol-Chloroform-Isoamyl Alcohol method, following Sambrook et al. (1989). Partial mitochondrial cytochrome b gene was amplified using primer CytbF700 (5'-CTTCCAACACCAAYCAAACATCTCAGCATGATGAAA-3') and CytbR700 (5'-ACTGTAGCCCCTCAGAATGATATTTGTCCTCA-3') published by Bauer et al. (2007). Polymerase Chain Reaction protocols were as followed by Mirza and Patel (2017). The PCR product was cleaned, and sequenced with a 3730 DNA Analyzer after cleaning. The sequence was cleaned manually in MEGA7 (Kumar et al. 2016). In order to ascertain phylogenetic position of the new species, published sequences were retrieved from GenBank used by Lajmi et al. (2016) listed in Appendix I. Sequences were aligned in Mega7 using ClustalW (Thompson and Gibson 2002) with default settings. For optimal partitioning strategy and evolutionary substitution model, aligned data was analyzed using PartitionFinder v.1.1.1 (Lanfear et al. 2012). Maximum Likelihood method was implemented to assess phylogenetic relationship with RAxML (Silvestro and Michalak 2012). Data were partitioned into three codons and GTR+G was used as the sequence substitution model, based on the optimal partitioning scheme suggested by PartitionFinder. Maximum likelihood analysis was run for 1,000 non-parametric bootstrap replicates with rapid ML search option. Sequence divergence uncorrected “p-distance” was calculated in Mega7. Sequence for the new species has been deposited with GenBank accession number “KX044190” for the specimen NCBS AT110.

Species delimitation: Bayesian Poisson Tree Process (bPTP) based on evolutionary placement algorithm was implemented using the web server (<http://species.h-its.org/ptp/>) following Zhang et al. (2013) for inferring putative species. Maximum likelihood tree was supplied for the analysis. Outgroup, *Hemidactylus frenatus*, was ex-

cluded from the analysis for optimum results. The analysis was run for 100,000 generations with three chains and 25% of the trees were discarded as burn-in. Results of the analysis are presented in Appendix III and Appendix IV.

Systematics

Hemidactylus chipkali sp. nov.

Fig. 1–5, Table 1.

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Holotype: NCBS AT107, adult male, from a cliff along the road leading to Pachmarhi town, Hoshangabad District, Madhya Pradesh (22.485050°, 78.449340°, 1,092 m). Collected on 09 May 2014 by Rajesh Sanap, David Raju, and Zeeshan Mirza.

Paratypes (four specimens): NCBS AT109 and BNHS 2426, adult males; NCBS AT108 and BNHS 2427, adult females, same data as holotype.

Diagnosis: A moderate sized species of the genus measuring 54.3–74.2 mm; TRL/SVL 36–43.6%; HL/SVL 26–31%; ear opening oval; anterior postmental width equal to first infralabial; posterior postmental width equal to second infralabial, posterior postmental not in contact with first infralabial; enlarged, keeled, tubercles, fairly regularly arranged in 15–16 longitudinal rows on dorsum; two angular series of seven precloacal femoral pores on each side separated by diastema of eight non-pored scales; non-pored scales equal to size of pored scales; scales bordering anterior edge of pored scales half the size of pored scales; five lamellae on digit I and seven (rarely eight) on digit IV of manus as well as pes; lamellae on digit IV and V of pes absent on basal ~25% of the digit; limbs long and slender FL/SVL 0.15 and CL/SVL 0.18; ventral aspect of tail with broad caudal scales covering ~80% of the tail; two subconical post cloacal spurs, anterior spur slightly larger than the posterior spur.

Etymology: The specific epithet “*chipkali*” is the Hindi word for gecko.

Description of holotype male NCBS AT107: Holotype in good condition preserved in a linear manner with a slightly curved tail. Hemipenis partly everted. Over half of the tail regenerated (Fig. 1A, B).

A medium sized gecko (SVL 59 mm) with a fairly large head (HL/SVL ratio 0.23), head slightly longer than wide (HW/HL ratio 0.92), head slightly depressed (HH/HL ratio 0.48), distinct from neck (Fig. 2A); canthus rostralis slightly inflated; snout short (SE/HW ratio 0.57), obtusely pointed from dorsal view and acutely in lateral view (Fig. 2B), longer than eye diameter (OD/SE ratio 0.55); scales on the snout subequal, convex, those anterior to the eye and on canthus rostralis, larger than the surrounding scales; eyes large (OD/HL ratio 0.29), pupil vertical with crenulated edges; supraciliaries smaller on



Fig. 1. *Hemidactylus chipkali* sp. nov. male holotype NCBS AT107, (A) dorsal view, (b) ventral view.

the anterior edge of the orbit, gradually increasing in size as they progress towards upper surface of the head; ear-opening large, sub-oval, obliquely oriented, its length at its greatest extent thrice that of the orbital diameter (EL/OD ratio 0.30) bearing three lobules on its anterior inner wall; eye to ear distance greater than diameter of eye (EE/OD ratio 1.11); rostral quadrangle, much wider than deep, divided by a median suture for its entire length; rostral in contact with nasal, first supralabial and internasals; two large and a slightly smaller internasals between nasals; mental triangular, wider (3.2) than long (2.8); two pairs of postmentals, anterior postmental longer (2.6) than wide (1.8); posterior pair of postmental slightly smaller than anterior pair, longer (2.3) than wide (1.4); anterior postmental in contact with mental, infralabials and posterior pair of postmental; posterior postmentals separated by five scales; anterior postmental equal in width to the first infralabial; posterior postmental equal to width of second infralabials (Fig. 2C); scales on throat circular, smaller than the ones ventral aspect of trunk; supralabials (to midorbital position) nine on left and ten on right side; supralabials (to angle of jaw) eleven on left side and twelve on right side; infralabials (to angle of

jaw) nine on left and ten on right side.

Body elongate (TRL/SVL ratio 0.45) and dorsoventrally flattened, more so after preservation; lacking distinct ventrolateral furrow; dorsal scalation on trunk granular intermixed with enlarged, keeled, tubercles, fairly regularly arranged in 15–16 longitudinal rows; dorsal tubercles on mid-dorsum longer (1.0) than wide (0.9); individual tubercle row separated from the adjacent by three transverse scale rows and by preceding tubercle of the same row, by four scale rows (Fig. 3A); ventral scales on trunk smooth, flat, larger than dorsal scales; mid body scales across belly 28–30 (Fig. 1B); eight (left) and seven (right) femoral pores separated at mid-pelvic region by eight non-pored scales; non-pored scales slightly larger than pored scales (Fig. 3B).

Limbs moderately long, slender; digits dilated, bearing slightly oblique lamellae on ventral surface; clawed, claw nearly half the length of the lamellar region; forelimbs short (FL/SVL ratio 0.15), slightly shorter than hind limbs (CL/SVL ratio 0.18), all digits of manus and digits I–IV of pes indistinctly webbed at the base. Terminal phalanx of all digits curved, arising angularly from distal portion of expanded lamellar pad, free portion of

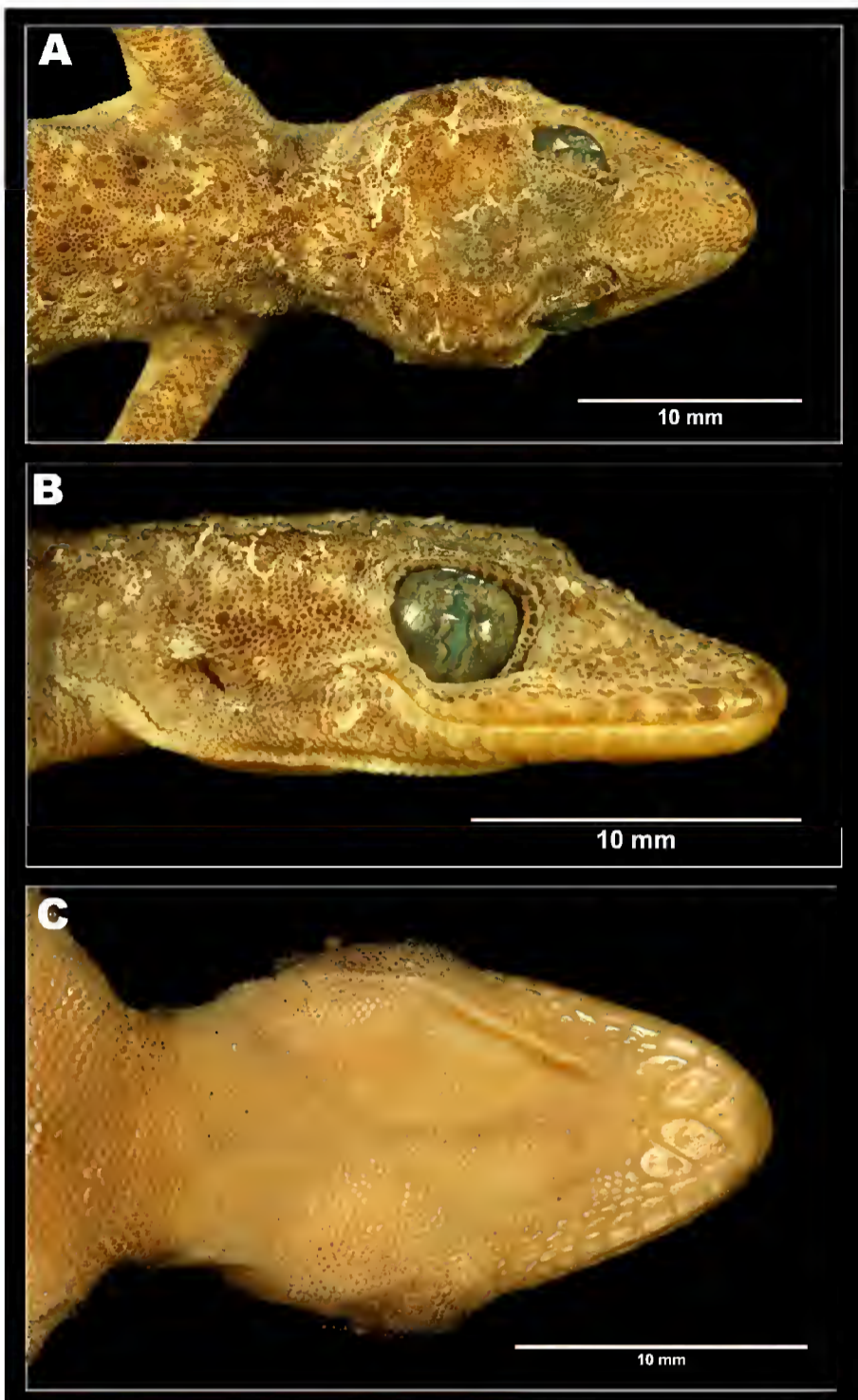


Fig. 2. *Hemidactylus chipkali* sp. nov. male holotype N.CBS AT107 head, (A) dorsal view, (B) lateral view, (C) ventral view.

phalanx of all digits half to more than half long as the dilated portion. Lamellae beneath the digits, left manus 5-6-7-7-6, right manus and left pes 5-7-7-7-7 (Fig. 4A), right pes 5-7-8-7-6 (Fig. 4B). Lamellae not reaching the base of the digit IV of pes. Relative lengths of digits: III>IV=V>II>I (right manus), IV>II=III>V>I (right pes). Tail moderately depressed, oval in cross section, longer than snout-vent length (TL/SVL ratio 1.26), 59.4 mm of the tail regenerated. Caudal segments distinct; pholidosis of original tail dorsum with small, juxtaposed scales intermixed with large depressed keeled tubercles, scales on regenerated portion of tail with slightly larger scales and lacking tubercles. First tail segment with a whorl of ten large conical, keeled tubercles, second segment onwards, each segment with six tubercles. Ventral aspect with large, broad scales covering about ~80% of the tail width from base of tail to the tip (Fig. 3C). Two subconical post cloacal spurs, anterior spur slightly larger than the posterior spur.

Coloration in life (Fig. 5): Coloration is a shade of pale brown with white and dark brown spots across the dorsum. Three adjoining brown spots over the nape and similar spots at a fairly regular distance from the preced-

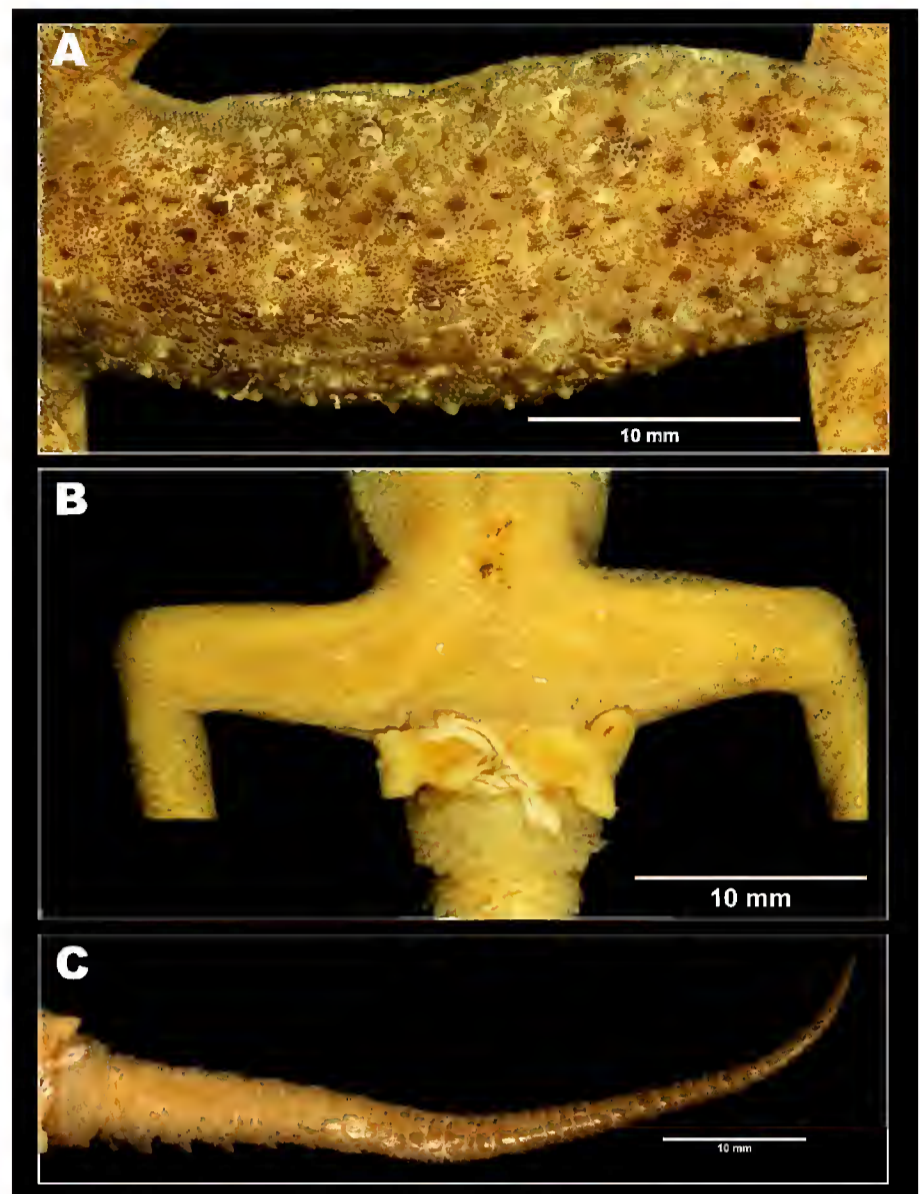


Fig. 3. *Hemidactylus chipkali* sp. nov. male holotype NCBS AT107, (A) dorsal view of trunk, (B) ventral view of cloaca showing precloacal femoral pores and hemipenis, (C) ventral view of tail showing enlarged sub-caudal scales.

ing row all through the trunk up to the flank. Each dark band is separated from the subsequent one by loosely connected white spots, to form thin white bands. Limbs pale brown with whitish spots all over the dorsum. Tail with alternate pale brown and cream colored bands. Coloration in preservative (Fig. 6): Specimens paler than in life with vestigial remains of dark brown spots and little to no trace of white spots on dorsum. Underparts straw colored.

Natural History: The new species was collected from vertical cliffs along a road leading to Pachmarhi situated in the Satpura Hills of central India (Fig. 7). Satpura Hills are located south of the Narmada River, running parallel to the river from western Gujarat through the borders of Maharashtra and Madhya Pradesh, extending up to northeastern Madhya Pradesh. The landscape at the type locality is undulating with the highest peak reaching 1,350 m and is dominated by tree species like *Tectona grandis* and *Shorea robusta*, characteristic of deciduous forests in the region. The hills at the type locality have steep cliffs where the new species was found (Fig. 8). All the type specimens and a few additional uncollected specimens were found actively moving on roadside rocks (Fig. 9). The species was observed to be sympatric with *Eublepharis satpuraensis*, which likely shares the crevices in the cliff during the day and emerges at dusk. Most individuals would dart towards the nearest crevice when

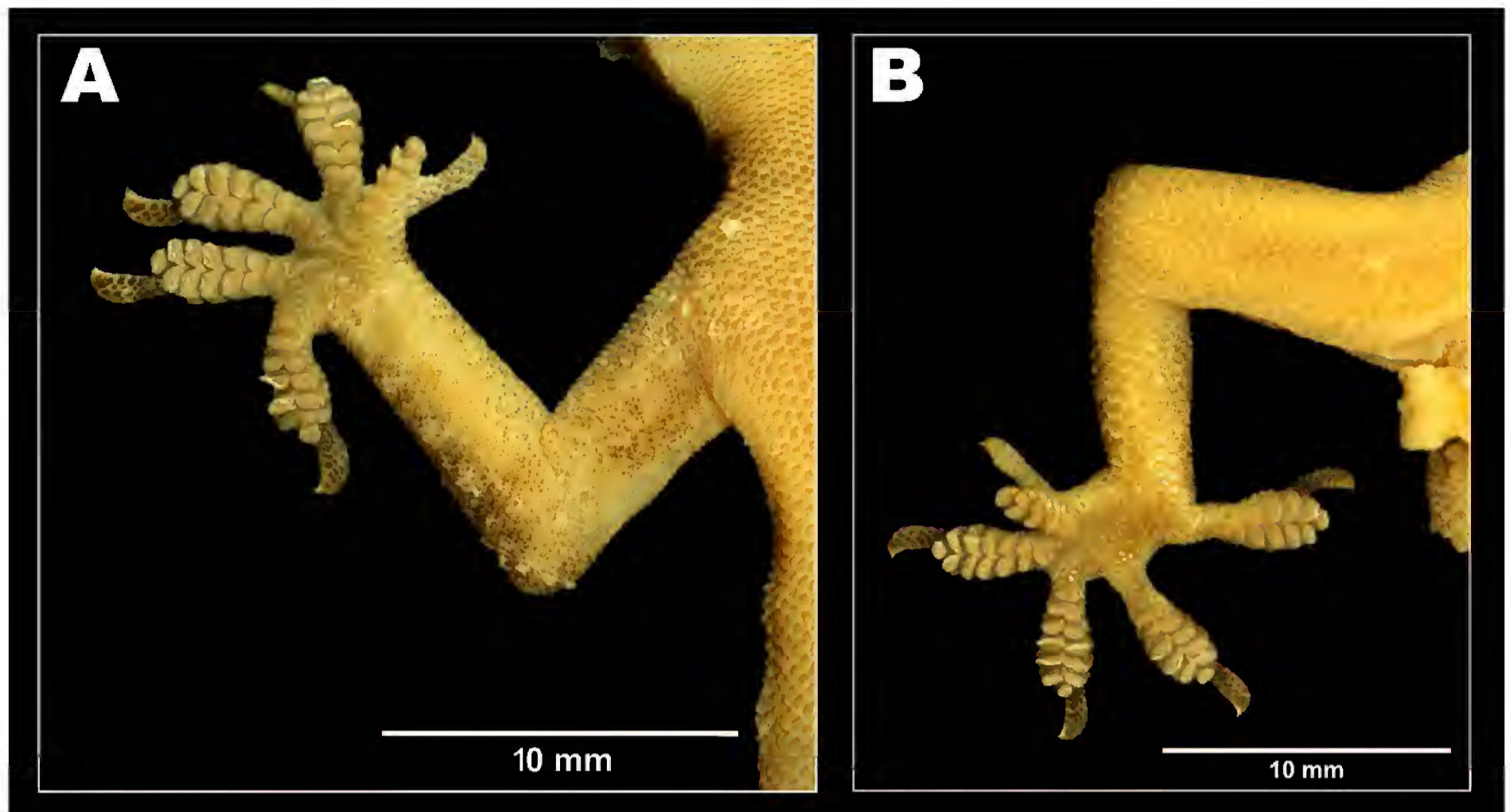


Fig. 4. *Hemidactylus chipkali* sp. nov. male holotype NCBS AT107 (A) right manus, (B) right pes.

approached with flashlights. The new species is likely restricted to these high elevation cliffs as only *H. cf. gleadowi* was recorded from near Bijakhori village, Sohagpur ca. 30 km (aerial distance, elevation 367 m) northwest of the type locality. One of the female paratypes (NCBS AT108) shows presence of two well-developed eggs within the body cavity suggesting that the species breed during the summer. With regards to its IUCN status, we recommend designating this species as “Data Deficient” in terms of its distribution, until further reports surface. During the course of the survey, no immediate threat to the species was observed and the entire area where the species was observed is protected as part of the Satpura Tiger Reserve. However, large parts of the Satpura hills are not protected and further surveys must be conducted to assess conservation threats to the species outside protected areas.

Suggested common name: Central Indian Leaf-toed Gecko.

Comparison: *Hemidactylus chipkali* sp. nov. differs from most Indian congeners in bearing the following set of differing and non-overlapping characters: SVL 54.3–74.2 mm (vs. SVL > 80 mm in *H. maculatus* Duméril and Bibron, *H. graniticolus* Agarwal, Giri, and Bauer, *H. giganteus* Stoliczka, *H. gujaratensis* Giri, Bauer, Vyas, and Patil, *H. prashadi* Smith, *H. acanthopholis* Mirza and Sanap, *H. aaronbaueri* Giri, *H. yajurvedi* Murthy, Bauer, Lajmi, Agarwal, and Giri), dorsum with keeled tubercles fairly arranged in 15–16 longitudinal rows (vs. tubercles absent or few or irregularly arranged in *H. aquilonius* Zug and McMahan, *H. flaviviridis* Rüppell, *H. frenatus* Schlegel, *H. garnotii* Duméril and Bibron, *H.*

leschenaultii Duméril and Bibron, *H. hemchandrai* Dandge and Tiple), presence of seven femoral pores separated medially by a diastema of eight non-pored scales (vs. precloacal pores in *H. sataraensis* Giri and Bauer, *H. gracilis* Blanford, *H. reticulatus* Beddome, *H. albofasciatus* Grandison and Soman, *H. scabriceps* Annandale, *H. persicus* Anderson, *H. robustus* Heyden, *H. turcicus* Linnaeus), dorsal tubercles sub-triangular (vs. tubercles triangular in *H. triedrus* Daudin and *H. subtriedrus* Jerdon), lacking webbing on hind feet and a fringe of skin on lateral aspect of tail (vs. present in *H. platyurus* Schneider), lamellae divided (undivided in *H. anamallensis* Günther).

Hemidactylus chipkali sp. nov. is most similar to members of the *Hemidactylus brookii* group and is here compared with taxa considered valid by Mahony (2011) and Kathriner et al. (2014). *Hemidactylus chipkali* sp. nov. differs from *H. brookii* (as defined by Mahony 2011) in larger SVL 74 mm (vs. SVL 55.8 mm in *H. brookii*, SVL 43.1 mm in *H. gleadowi* Murray, SVL 45–51.4 mm in *H. kushmorensis* Murray, 51.5 mm in *H. parvimaculatus* Deraniyagala); anterior postmental width equal to first infralabial; posterior postmental width equal to second infralabial, posterior postmental not in contact with first infralabial or with narrow contact Figs. 10A–E (vs. width of posterior postmental shorter than width of second infralabial in *H. brookii*, width of posterior postmental shorter than width of second infralabial, posterior in contact with first infralabial in *H. gleadowi*, anterior, posterior postmental in broad contact with first infralabial in *H. kushmorensis*, width of anterior postmental longer than first infralabial, and anterior postmental in contact with first and second infralabials in *H. treutleri* Mahony); seven precloacal femoral pores separated medially by a

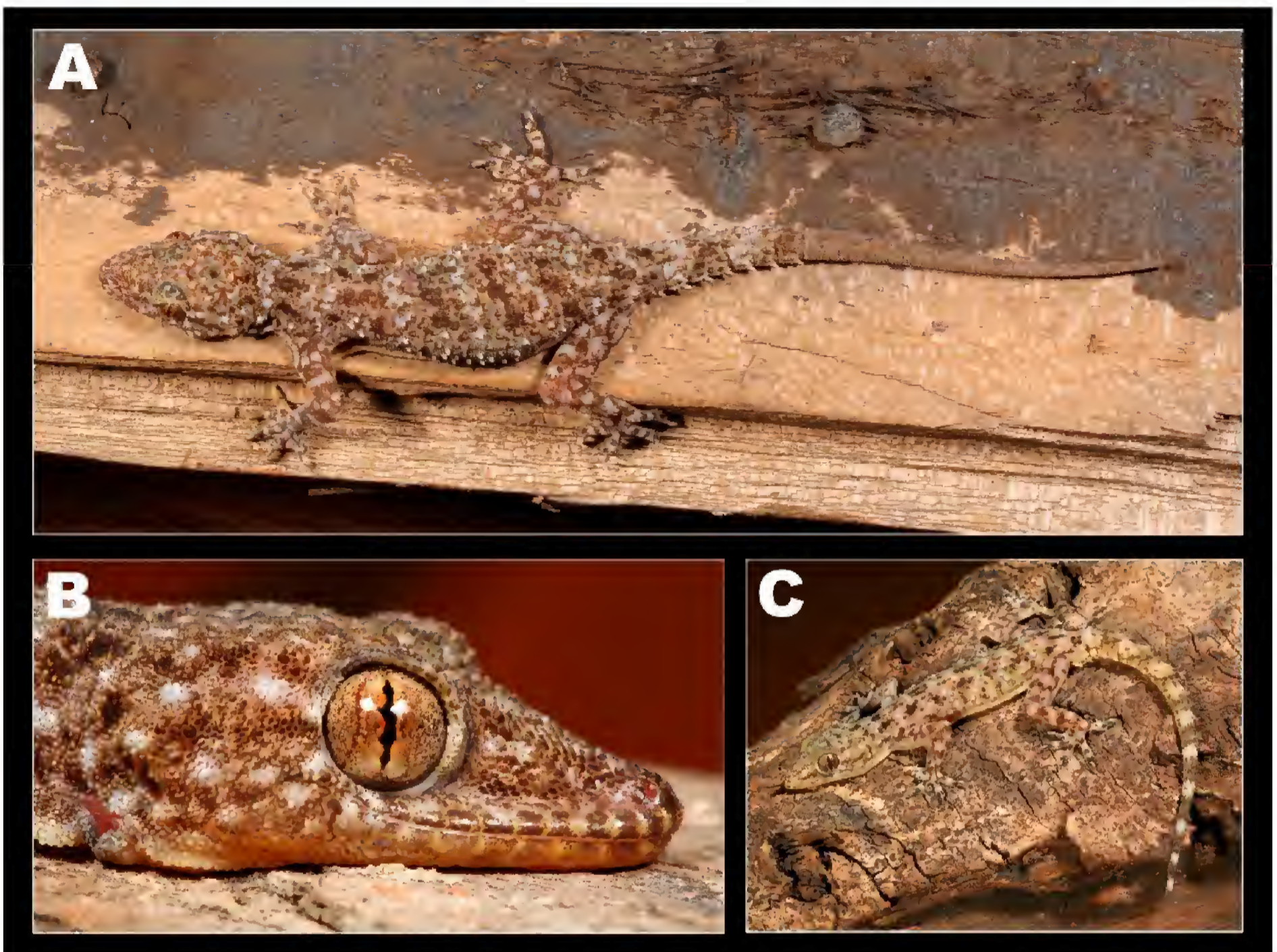


Fig. 5. *Hemidactylus chipkali* sp. nov. (A and B) male holotype NCBS AT107 in life, (C) male paratype NCBS AT108 in life.



Fig. 6. Dorsal aspect of the type series showing coloration after preservation.

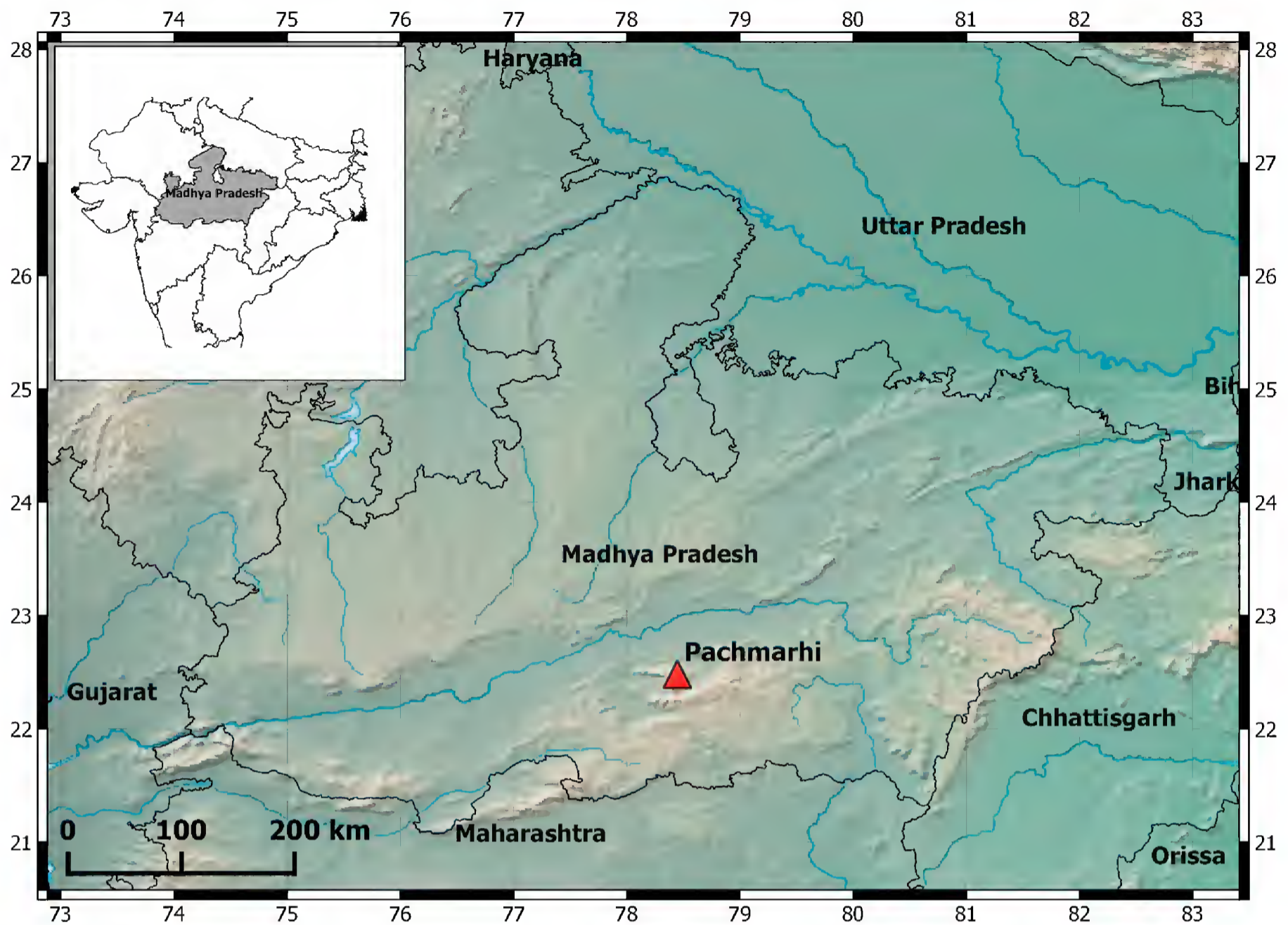


Fig. 7. Map of Madhya Pradesh, central India, showing the type locality Pachmarhi (indicated by a red triangle). Inset map shows location of Madhya Pradesh in India.



Fig. 8. Biotope of Satpura hills showing characteristic rocky cliffs and forest cover where the new species was collected.



Fig. 9. Rocks along the road leading to Pachmarhi town where the type specimens were collected.

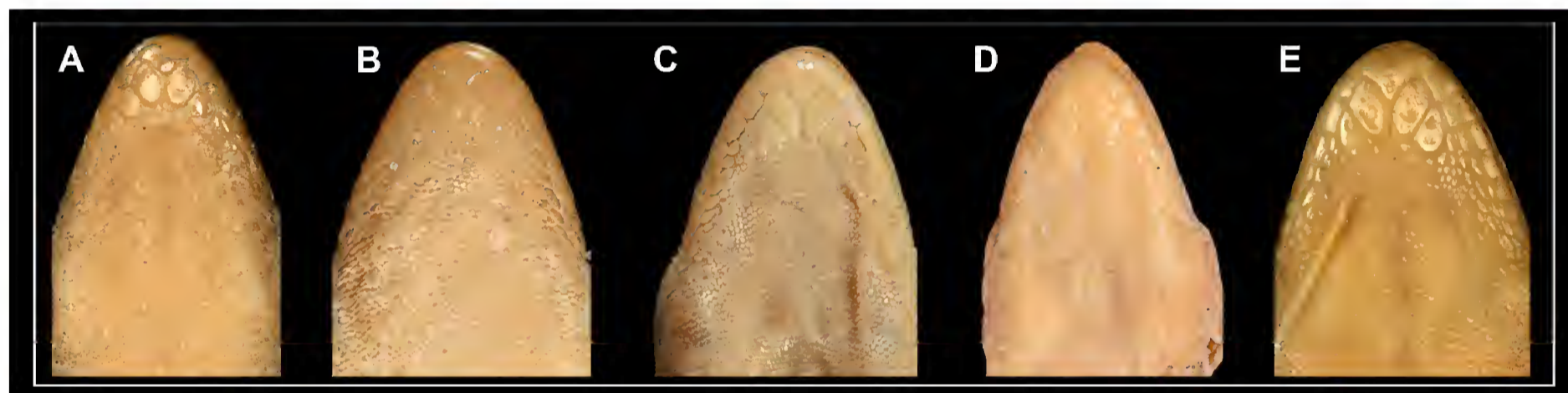


Fig. 10. Ventral view of head, (A) *H. cf. gleadowi* NCBS HA-107, (B) *H. cf. murrayi* NCBS HA-110, (C) *H. subtriedroides* lectotype NHM 1946.8.2554, (D) *H. treutleri* holotype ZSI 25711, (E) *H. chipkali* sp. nov.

diastem of eight non-pored scales Figs. 11A–E (vs. 12–13 precloacal femoral pores separated medially by a diastem of one non-pored scale in *H. brookii* and *H. gleadowi*, 10–11 precloacal femoral pores separated by 2–3 non-pored scales in *H. kushmorensis*, 12–15 pores separated by 2–4 non-pored scales in *H. parvimaculatus*, 7–8 separated by 5–6 non-pored scales in *H. subtriedroides* (Anandale); lamellae series on digit IV do not extend to base Figs. 12A–C (vs. lamellae series cover the entire digit IV in *H. brookii*, *H. cf. murrayi* Gleadow, *H. subtriedroides*, *H. tenkatei* Lidth de Jeude, *H. treutleri* and *H. kushmorensis*); scales bordering anteriorly the precloacal pores half the size of pored scales (vs. scales bordering anteriorly the precloacal pores \geq the size of pored scales in *H. brookii*); keeled dorsal tubercles in 15–16 fairly longitudinal rows (vs. 19–20 in *H. kushmorensis*); five lamellae on digit I of pes (vs. 6–7 in *H. treutleri*); lamellae on digit IV of pes 7 rarely 8 (vs. 10 in *H. kushmorensis*, 8

in *H. cf. murrayi*, 9 in *H. treutleri*, 11 in *H. mahendrai* Shukla); caudal plates enlarged and cover \sim 80% of the underside of the tail (vs. tail plates not covering entire tail in *H. gleadowi*, *H. kushmorensis*, *H. subtriedroides*, *H. tenkatei*); two sub-conical postcloacal spurs, anterior or one slight larger than the posterior (vs. 2–3 medium sized with or without an additional large spur in *H. subtriedroides* and *H. cf. murrayi*, two very small ones in *H. gleadowi*, a single domed spur in *H. kushmorensis*, three enlarged spurs in *H. treutleri*); sub-caudal completely transverse the tail width (sub-caudal not as enlarged as in *H. gleadowi*, *H. kushmorensis*, *H. subtriedroides*, *H. tenkatei*, *H. brookii*, *H. cf. murrayi*), FL/SVL 0.15 (vs. 0.13 in *H. kushmorensis*, *H. subtriedroides*, *H. brookii*, 0.12 in *H. gleadowi*, *H. cf. murrayi*); CL/SVI 0.18 (vs. 0.15 in *H. brooki*, *H. gleadowi*, 0.14 in *H. kushmorensis*, 0.16 in *H. tenkatei*, *H. subtriedroides*).

Discussion and Conclusion

Phylogenetic relationships within Indian and South Asian *Hemidactylus* have been the subject of recent studies (Bansal and Karanth 2010; Bauer et al. 2010b). However, due to lack of extensive sampling in most studies, the *H. brookii* complex remained unresolved and still does. Kathriner et al. (2014) provided new insights on

the systematics of the *H. brookii* complex, which raises doubts on previous assumptions and results based solely on morphology. Lajmi et al. (2016) presented the first ever comprehensive analysis of *H. brookii* complex incorporating molecular as well as morphological data which has enhanced our understanding of this group thus enabling us to present preliminary data on phylogenetic relationship of the new species. Based on a short fragment of ~302 bp of mitochondrial *cyt b* gene, the new species appears to be allied to *H. treutleri* (Fig. 13) and is a member of clade 5 of Lajmi et al. (2016). It however differs in having an uncorrected p-distance of 14–16% (Fig. 14, Table 4). The phylogenetic analysis results presented here are preliminary, based on data generated by Lajmi et al. (2016). Publication by Lajmi et al. (2016) contains 30 accession numbers, which are repeats and is likely a typographical error. The authors have not copied accession number correctly from previous studies and have the same accession numbers for several sequences of specimens from different localities. It is hoped that the authors provide correct accession numbers and their respective voucher details in a subsequent paper.

Relationships recovered from molecular phylogenetics shows discordance with morphology in the new species, showing close affinity to *H. cf. murrayi* based on morphology whereas it shows affinity to *H. treutleri* based on molecular data. The new species however differs from *H. treutleri* and *H. cf. murrayi* in having broad sub-caudals transverse the entire width of the tail and in bearing 7 lamellae on fourth toe vs. 8 in *H. cf. murrayi* and 9 in *H. treutleri*. Principal Component Analysis of data including morphometric data for the new species, *H. treutleri* and *H. cf. murrayi* for standardized morphometric data showed PC1 + PC2 explaining 80% + 16% of variance, respectively (Fig. 14, Appendix II). Plot of the first two principal axes resulted in two clusters; one of *H. chipkali* and another one of *H. treutleri* and *H. cf. murrayi* (Fig. 15). Results from bPTP support the distinctiveness of the species with high support (Appendix III and IV).

Hemidactylus murrayi Gleadow, 1887 was described based on a series of 24 specimens from “Pimpri and Garvi, in the Dangs” in southern Gujarat. The types are like-

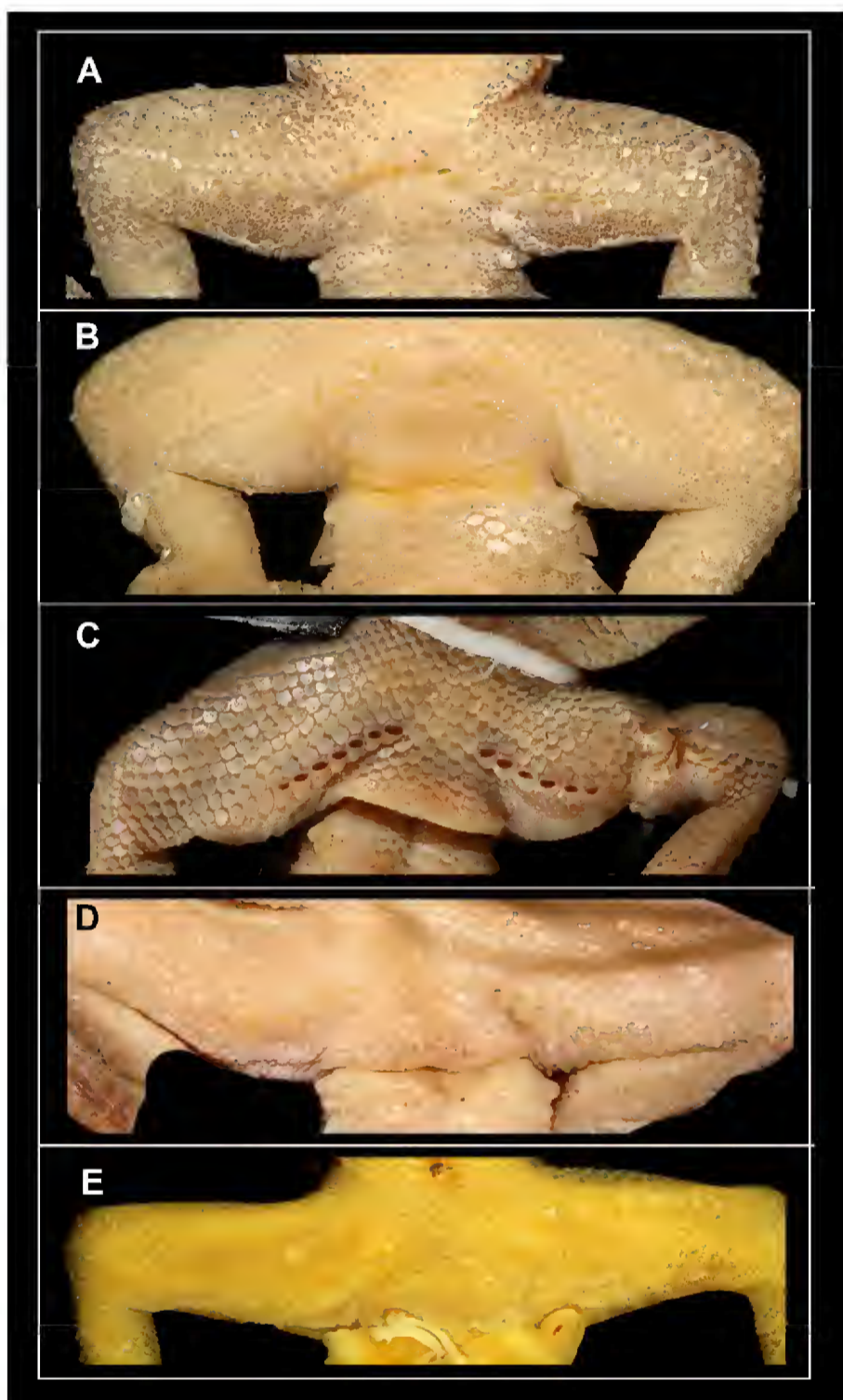


Fig. 11. Preloacal and or femoral pores, (A) *H. cf. gleadowi* NCBS HA-107, (B) *H. cf. murrayi* NCBS HA-110, (C) *H. subtrianguloides* lectotype NHM 1946.8.2554, (D) *H. treutleri* holotype ZSI 25711, (E) *H. chipkali* sp. nov.



Fig. 12. Ventral aspect of right pes, (A) *H. cf. gleadowi* NCBS HA-107 note lamellae on digit IV not reaching base, (B) *H. cf. murrayi* NCBS HA-110 lamellae covering entire digit IV, (C) *H. chipkali* sp. nov. Note lamellae on digit IV not reaching base.

A new gecko of the genus *Hemidactylus*

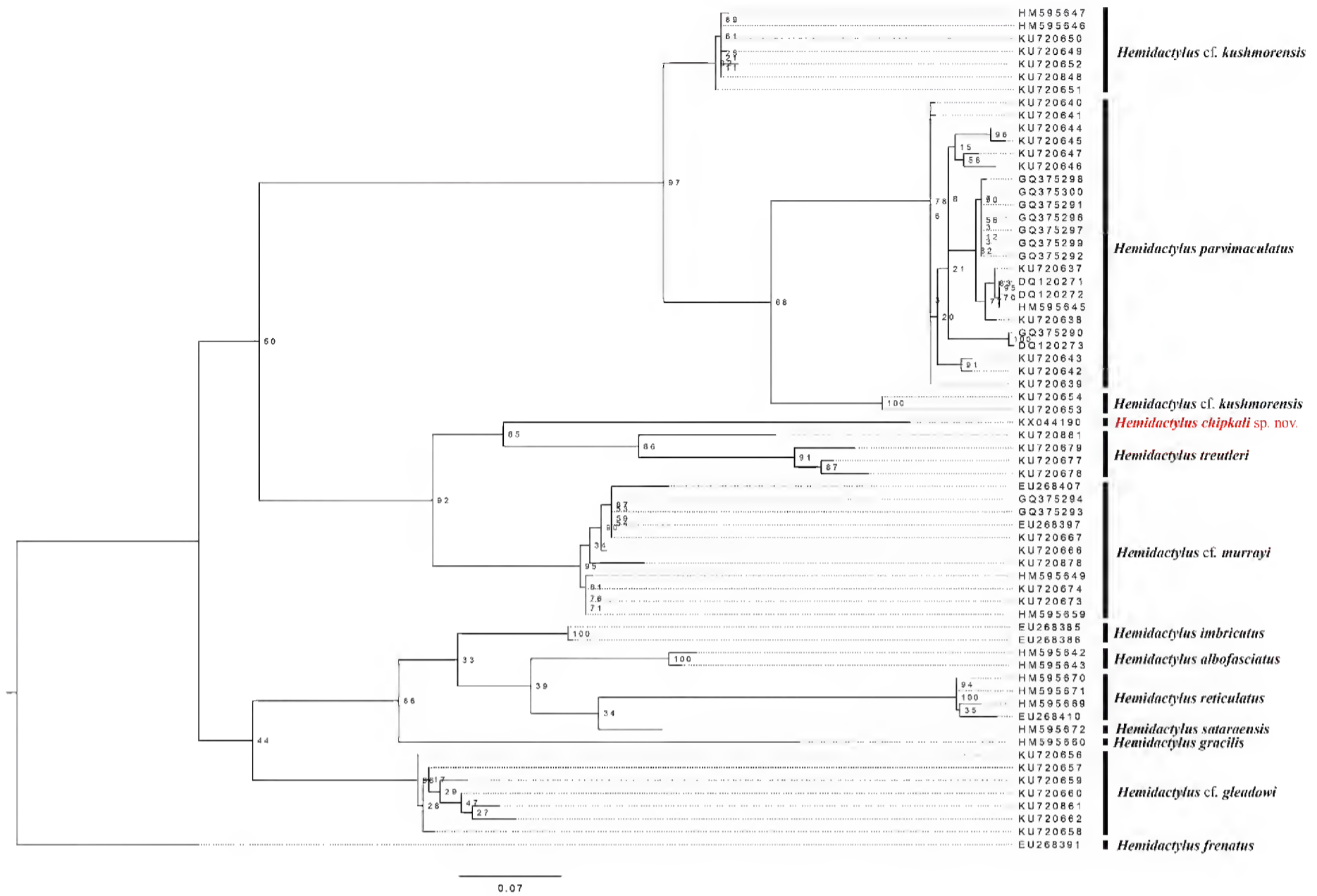


Fig. 13. Maximum likelihood tree for selected members of the *H. brookii* group showing relationship of *H. chipkali* sp. nov. rooted with *H. frenatus* as outgroup based on ~302 bp of mitochondrial cytochrome *b* gene with 1,000 non-parametric bootstrap replicates. Numbers at nodes indicate bootstrap support.

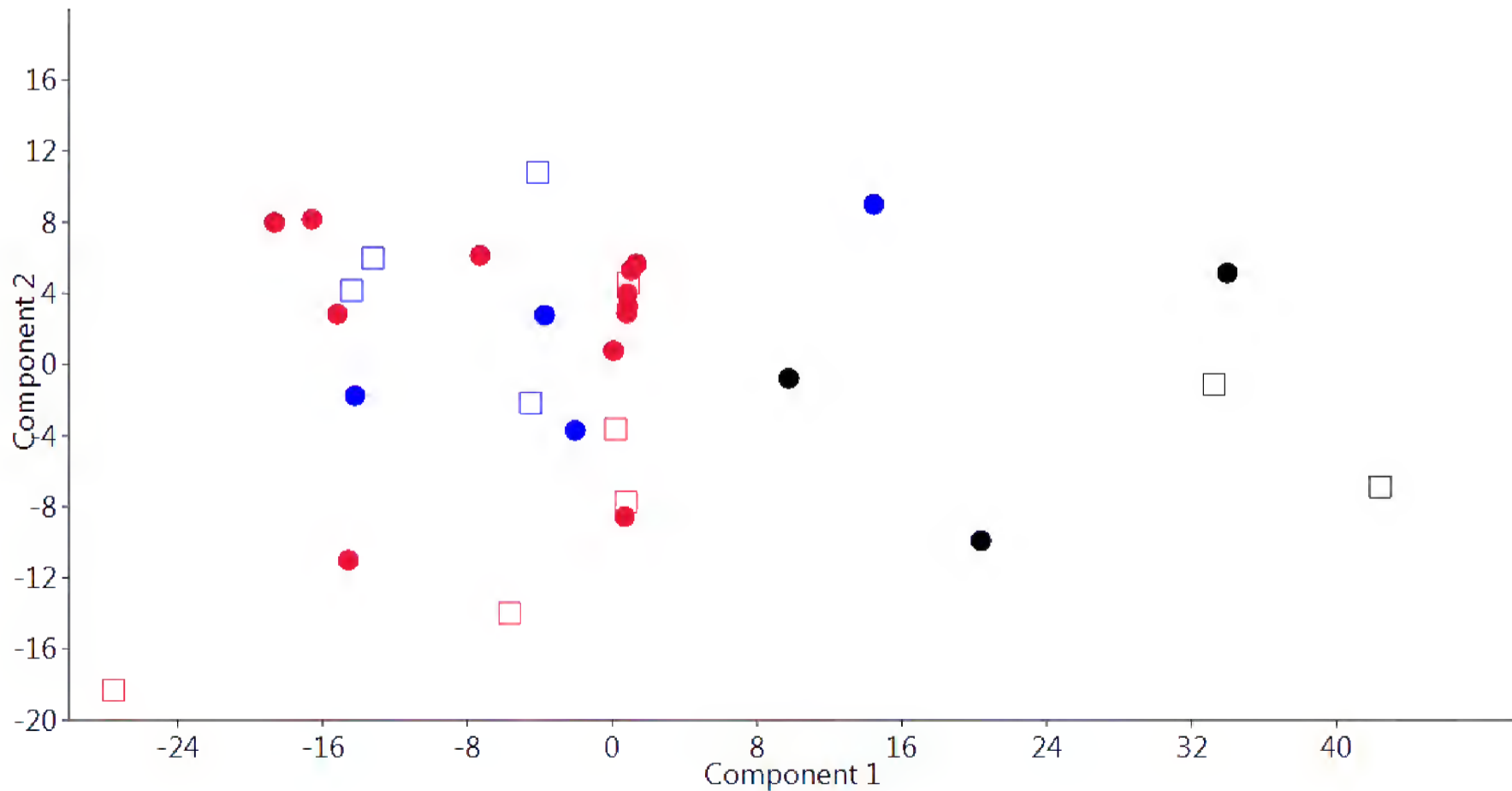


Fig. 14. PCA plot for standardized morphometric data for *H. chipkali* sp. nov. (black), *H. cf. murrayi* (red) and *H. treutleri* (blue). Circles = male and squares = female.

ly lost and hence the identity of the species can only be ascertained after examination of material from both the said localities. Lajmi et al. (2016), who considered clade 4 of their work as *H. murrayi*, however do not include molecular data from either of the localities from where types of *H. murrayi* were collected. *Hemidactylus tenkatei* was found nested in clade 4 of Lajmi et al. (2016), suggesting that this clade might represent more than one species. To further support this, a sample from Nashik (GenBank accession number KU720676) in clade 4 of Lajmi et al. (2016) shows ~8% sequence divergence for cytochrome *b* from other members of the clade which may represent yet another undescribed taxon (Appendix V). Results from bPTP suggests that *H. treutleri* likely is a species complex (Appendix III and IV). In order to resolve this group, a neotype for *H. murrayi* and *H. mahendrai*, each, must be designated and molecular data for the neotypes/topotypes must be incorporated in a phylogeny, and also molecular data from the type locality of *H. subtriedroides* Annandale (suggested to be a valid species by Kathriner et al. 2014), which will shed light on the systematics of this clade that we refer to as *H. cf. murrayi* in the present work. Considering that members of the *H. cf. murrayi* clade are commensal, it may not be an easy task to resolve this complex, largely due to multiple back and forth colonizations in recent years through human agencies.

Description of yet another member of the *H. brookii* complex highlights the diversity of the *H. brookii* complex in India. Including the present description, at least seven species of the *H. brookii* complex have been recorded from India including *H. mahendrai* (see Lajmi et al. 2016). India and Sri Lanka are home to several endemic species of *Hemidactylus* (Bauer et al. 2010b). This number is steadily increasing with dedicated surveys, as well as re-examination of museum specimens (Agarwal et al. 2011; Mirza and Sanap 2014). Explorations of isolated and/or unexplored hill ranges like the Satpura hills, Aravalli hills, and other small hills across the country would certainly harbor undocumented species of reptiles as demonstrated by the discoveries of *Cyrtodactylus srilekhae*, *C. rishivalleyensis*, *C. varadgirii* (Agarwal 2016, Agarwal et al. 2016), *Eublepharis satpuraensis* (Mirza et al. 2014), *H. chipkali* sp. nov., *H. sataraensis* (Giri and Bauer 2008), and *Wallaceophis gujaratensis* (Mirza et al. 2016). Our finding further attests the poor nature of reptilian documentation in the country and the lack of taxonomic revisions on most reptilian groups (see Gowande et al. 2016, Mirza and Sanap 2014, Mirza et al. 2010).

Acknowledgments.—This herpetofaunal documentation project would not have been possible without necessary permits granted by the forest department of Madhya Pradesh for which we are grateful to Narendra Kumar (PCCF, Wildlife and Chief Wildlife Warden), Ravi Shrivastava (PCCF Wildlife), R.P. Singh (APCCF Wildlife),

Anil Nagar (Field Director, Satpura Tiger Reserve), and Dr. Suhas Kumar for necessary permissions to carry out research in Madhya Pradesh. We thank Tulika Kedia and Singinawa Conservation Foundation for all their help and support. We also thank Forsyth Lodge for logistic support and permission to conduct surveys on their property. Rahul Khot (BNHS, Mumbai), Kaushik Deuti (ZSI, Kolkata), and Patrick Campbell (NHM, London) helped with access to type specimens. Special thanks goes to Anurag Mishra (NCBS) for reviewing the final draft of the manuscript. Harshil Patel provided valuable input on *H. cf. murrayi* for which we kindly acknowledge him. Rajesh Sanap and Surya Ramachandran in addition helped with fieldwork. Krushnamegh Kunte granted permission and access to lab facilities at the National Centre for Biological Sciences. Fieldwork was supported by a generous grant from the Rufford foundation to ZM. Special thanks to Robin K. Abraham for constructive comments on the final draft of this paper. Finally, I. Das and Ishan Agarwal provided valuable comments from which the manuscript greatly benefitted.

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David V. Raju comes from a small village called Kuzhimattom in Kottayam District of Kerala, India. He graduated from Baselius College Kottayam in English Literature. David has always had an interest in wildlife and further developed his interest at the Kottayam Nature Society. Currently he is working as a naturalist in Central India. He has co-authored a book on the dragonflies of Kerala. He was also a part of the team which discovered ten frogs in Western Ghats and a leopard gecko from Satpura hills. His other interests are birds, butterflies, and mammals.

Comperative material examined:

- Hemidactylus aaronbaueri*: Holotype BNHS 1739 (male), Ghatghar, Taluka Junnar, Pune District, Maharashtra, India; ZSI 21648A and ZSI 21648C (female), ZSI 21648B (male), Bhairavgadh Fort, Taluka Karjat, Pune District, Maharashtra, India.
- Hemidactylus acanthopholis*: Holotype NHM 1946.8.23.68 (male), paratypes NHM 1946.8.2367 (male), Tirunelveli District, Tamil Nadu.
- Hemidactylus albofasciatus*: Paratype ZSI 21109 (female), Dorle village, Rajapur Taluka, Ratnagiri District, Maharashtra, India; two males BNHS 1579 and 1582 Dabhil-Ambere, Ratnagiri District, Maharashtra, India.
- Hemidactylus bengaliensis* Anderson (= *H. flaviviridis*): Syntype ZSI 5780, Bengal.
- Hemidactylus flaviviridis*: ZSI 20963 (male) Jaipur, Rajasthan, India; ZSI 21688 (female) Udaipur, Rajasthan, India.
- Hemidactylus hunae*: Type specimen NHM 1946.8.23.77 (female), Okanda, Eastern Province, Sri Lanka.
- Hemidactylus giganteus*: Syntype, NHM 1877.8.6.5 (male), Godavari valley near Bhadrachalam, Andhra Pradesh, India.
- Hemidactylus* cf. *gleadowi*: Male NCBS HA-107 Khamgaon, Maharashtra; male NCBS HA-108 Sohagpur, Madhya Pradesh.
- Hemidactylus gracilis*: Syntype, ZSI 5190 (male), from “S.E. Berár” (in Madhya Pradesh, India; BNHS 1591 (male) and BNHS 1592 (female), Chatusringi hills, Pune, Maharashtra, India.
- Hemidactylus graniticolus*: Holotype BNHS 1850 (female), hills near Harohalli, Bangalore Rural district, Karnataka, India; paratypes NHM 1946.8.23.70 (female), NHM 1946.8.23.71 (female), NHM 1946.8.23.72 (male), NHM 1946.8.23.73 (female), NHM 1946.8.23.74 (female), NHM 1946.8.23.75 (female), Salem District, Tamil Nadu, India; NHM 1946.8.23.76 (male), “Malabar,” India.
- Hemidactylus gujaratensis*: Holotype BNHS 1818 (female) Vagheshwari Mata Temple, Junagadh City, Junagadh District, Gujarat, India.
- Hemidactylus kelaartii*: Syntypes ZSI 2617 (male) and ZSI 2618 (female), from “Ceylon” (= Sri Lanka).
- Hemidactylus maculatus*: NHM 1956.1.11.41 (female), Matheran, Raigad District, Maharashtra, India; ZSI 25608 (male) Government rest house, Panchagani, Satara District, Maharashtra, India; BNHS 74 (female) and BNHS 75 (female), Mumbai, Maharashtra, India; BNHS 1086 (male), Kanheri caves, Mumbai, Maharashtra, India.
- Hemidactylus marmoratus* (= *Hemidactylus leschenaulti*): Holotype, ZSI 5058, from “S.E. Berár, near Chánda” Maharashtra, India.
- Hemidactylus* cf. *murrayi*: BNHS 1947–1948 (males), BNHS 1949 (female), Aarey Milk Colony, Mumbai, Maharashtra.
- Hemidactylus persicus*: Holotype, ZSI 5961, from “Persia” (= Iran). The register lists the type as from “Shiraz, Persia.”
- Hemidactylus platyceps* (= *Hemidactylus gracilis*): Holotype, ZSI 17020, from “Bilimora, Bombay Presidency” Gujarat, India.
- Hemidactylus prashadi*: BNHS 147 (male), Shirol forest, Belgaum North Kanara, Karnataka, India; BNHS 146 (male), Gersoppa falls, North Kanara, Karnataka, India; ZSI 20123 (female) neighbourhood of Jog, North Kanara district, Bombay Presidency’ (at present in Karnataka, India).
- Hemidactylus reticulatus*: Type specimens NHM 1874.4.29.410 (male) and NHM 1874.4.29.411 (female), Kollegal, Karnataka, India.
- Hemidactylus sataraensis*: Holotype BNHS 1743 (female) Chalakewadi, Satara District, Maharashtra, India; paratype BNHS 1742 (female); non-type BNHS 2288 (male), BNHS 2289 (female), Chalakewadi, Satara District, Maharashtra, India.
- Hemidactylus scabriceps*: Type specimens, ZSI 15353, from “Rámanád,” Tamil Nadu, India.
- Hemidactylus* sp. (*H.* cf. *maculatus*/*H.* cf. *subtriedrus*): ZSI 24155 (female), Bastar District, Chhattisgarh, India; ZSI 25866 (male) Tyda railway station, Tyda, Vishakapatnam district, Andhra Pradesh, India; ZSI 25708 (male) Ganjam district, Odisha, India; a large male without locality and registration tag along with ZSI 25708.
- Hemidactylus sykesii* (= *H. maculatus*): Type specimen, NHM XXII.20a (male), Deccan, India (Donated by Indian Museum XXII.20a).
- Hemidactylus subtriedroides*: Syntype, NHM 1946.8.25.54/ ZSI 4135, “Tsagain, Upper Burma.”
- Hemidactylus treutleri*: Holotype ZSI 25711 (male), paratype ZSI 25712 (female), outer stone wall of Golconda Fort, Hyderabad, Andhra Pradesh, India.
- Hemidactylus triedrus*: ZSI 17054 (female) Travindrum, Kerala, India; ZSI 5852, ZSI 5853 (males), Bangalore, Karnataka, India; ZSI 21483, ZSI 21486 (males), Pune, Maharashtra, India.

A new gecko of the genus *Hemidactylus*

Appendix I. List of species and their sequence accession numbers for the gene cytochrome *b* used in the present study.

Species	Locality	Accession number
<i>Hemidactylus albofasciatus</i>	Dorle, Ratnagiri, Maharashtra, India	HM595642
<i>Hemidactylus albofasciatus</i>	Malvan, Sindhudurg, Maharashtra, India	HM595643
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Chikkabellapur, Karnataka, India	KU720656
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Ranebennur, Karnataka, India	KU720657
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Mysore, Karnataka, India	KU720658
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Bagalkot, Karnataka, India	KU720659
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Dapoli, Maharashtra, India	KU720660
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Ahmednagar, Maharashtra, India	KU720661
<i>Hemidactylus</i> cf. <i>gleadowi</i>	Iqbalgadh, Gujarat, India	KU720662
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Reasi, Himachal Pradesh, India	KU720648
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Dehradun, Uttarakhand, India	HM595646
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Chamba, Himachal Pradesh, India	KU720649
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Kangra-Jawalamukhi Road, Himachal Pradesh, India	KU720650
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Ajmer, Rajasthan, India	KU720651
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Baripada, Odisha, India	KU720652
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Jammu, India	HM595647
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Chotila, Gujarat, India	KU720653
<i>Hemidactylus</i> cf. <i>kushmorensis</i>	Mt. Abu, Rajasthan, India	KU720654
<i>Hemidactylus</i> cf. <i>murrayi</i>	Badlapur, Maharashtra, India	KU720666
<i>Hemidactylus</i> cf. <i>murrayi</i>	Mumbai, Maharashtra, India	KU720667
<i>Hemidactylus</i> cf. <i>murrayi</i>	Loagan Bunut National Park, Sarawak, Malaysia	GQ375293
<i>Hemidactylus</i> cf. <i>murrayi</i>	Mandalay Division, Myanmar	EU268407
<i>Hemidactylus</i> cf. <i>murrayi</i>	Yangon, Myanmar	GQ375294
<i>Hemidactylus</i> cf. <i>murrayi</i>	Empangon Air Hitam, Pulau Pinang, Malaysia	EU268397
<i>Hemidactylus</i> cf. <i>murrayi</i>	Palakkad, Kerala, India	HM595649
<i>Hemidactylus</i> cf. <i>murrayi</i>	Malshej Ghat, Maharashtra, India	KU720673
<i>Hemidactylus</i> cf. <i>murrayi</i>	Junagadh, Gujarat, India	KU720674
<i>Hemidactylus</i> cf. <i>murrayi</i>	Nasik, Maharashtra, India	KU720676
<i>Hemidactylus frenatus</i>	Sri Lanka, Rathegala	EU268391
<i>Hemidactylus gracilis</i>	Pune, Maharashtra, India	HM595660
<i>Hemidactylus gracilis</i>	Kolhapur, Maharashtra, India	HM595659
<i>Hemidactylus imbricatus</i>	Pakistan (captive specimen)	EU268386
<i>Hemidactylus imbricatus</i>	Pakistan (captive specimen)	EU268385
<i>Hemidactylus parvimaculatus</i>	Gandagan, Odisha, India	KU720637
<i>Hemidactylus parvimaculatus</i>	Polupalli, Tamil Nadu, India	DQ120272
<i>Hemidactylus parvimaculatus</i>	Tumkur, Karnataka, India	HM595645
<i>Hemidactylus parvimaculatus</i>	Mauritius	DQ120271
<i>Hemidactylus parvimaculatus</i>	Mampuri, Sri Lanka	GQ375292
<i>Hemidactylus parvimaculatus</i>	Dehikindagama, Sri Lanka	GQ375296
<i>Hemidactylus parvimaculatus</i>	Matale, Sri Lanka	GQ375298
<i>Hemidactylus parvimaculatus</i>	Gonaganara, Sri Lanka	GQ375297
<i>Hemidactylus parvimaculatus</i>	Kartivu, Sri Lanka	GQ375291
<i>Hemidactylus parvimaculatus</i>	Matale, Sri Lanka	GQ375299
<i>Hemidactylus parvimaculatus</i>	Tempitiya, Sri Lanka	GQ375300

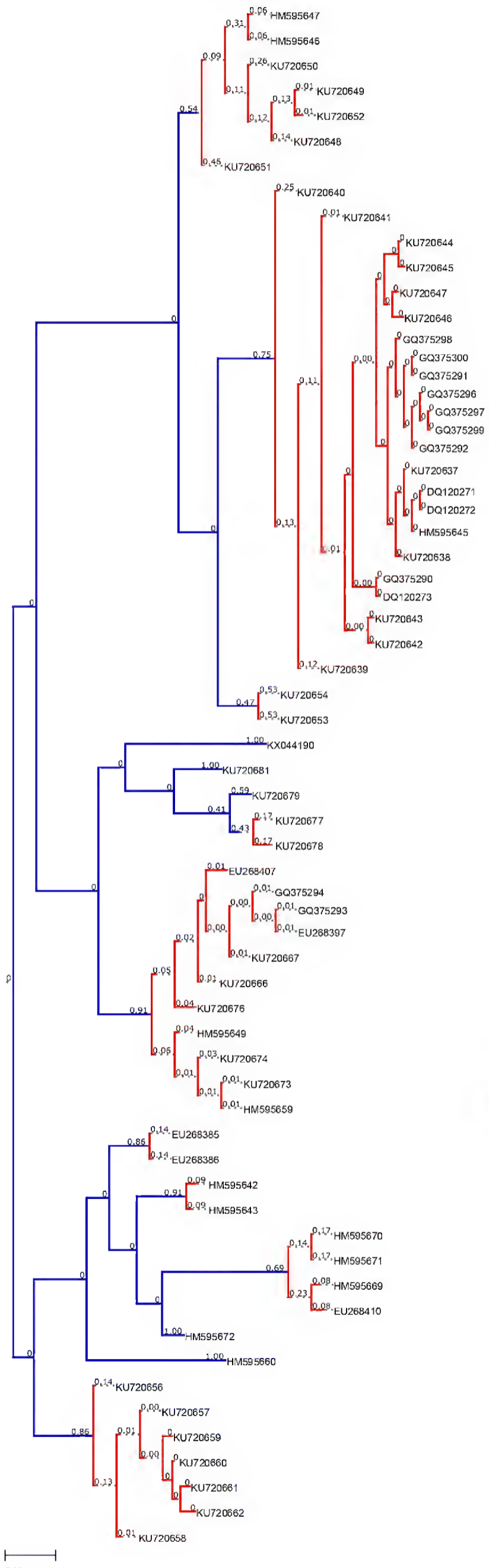
Appendix I (continued). List of species and their sequence accession numbers for the gene cytochrome *b* used in the present study.

Species	Locality	Accession number
<i>Hemidactylus parvimaculatus</i>	Rushikulya, Odisha, India	KU720638
<i>Hemidactylus parvimaculatus</i>	Attagulipura, Karnataka, India	KU720639
<i>Hemidactylus parvimaculatus</i>	Bangalore, Karnataka, India	KU720640
<i>Hemidactylus parvimaculatus</i>	Chennai, Tamil Nadu, India	KU720641
<i>Hemidactylus parvimaculatus</i>	Poinguinim, Goa, India	KU720642
<i>Hemidactylus parvimaculatus</i>	Mollem, Goa, India	KU720643
<i>Hemidactylus parvimaculatus</i>	Kutugam, Odisha, India	KU720644
<i>Hemidactylus parvimaculatus</i>	Araku Valley, Andhra Pradesh, India	KU720645
<i>Hemidactylus parvimaculatus</i>	Vizianagaram, Andhra Pradesh, India	KU720646
<i>Hemidactylus parvimaculatus</i>	Majhiguda, Odisha, India	KU720647
<i>Hemidactylus parvimaculatus</i>	Kollam, Kerala, India	DQ120273
<i>Hemidactylus parvimaculatus</i>	Kandy, Sri Lanka	GQ375290
<i>Hemidactylus reticulatus</i>	Pavgada, Karnataka, India	HM595669
<i>Hemidactylus reticulatus</i>	Nandi Hills, Karnataka, India	HM595670
<i>Hemidactylus reticulatus</i>	Nandi Hills, Karnataka, India	HM595671
<i>Hemidactylus reticulatus</i>	Vellore, Tamil Nadu, India	EU268410
<i>Hemidactylus satarauensis</i>	Chalakeswadi, Maharashtra, India	HM595672
<i>Hemidactylus treutleri</i>	Hyderabad, Telangana, India	KU720681
<i>Hemidactylus cf. treutleri</i>	Rishi valley, Andhra Pradesh, India	KU720679
<i>Hemidactylus cf. treutleri</i>	Kangudi, Tamil Nadu, India	KU720678
<i>Hemidactylus cf. treutleri</i>	Chikkabellapur, Karnataka, India	KU720677

Appendix II. PCA loadings for each character

	PC 1	PC 2
SVL	0.2125	0.7975
TRL	0.0613	0.3992
BW	0.0326	0.1582
CL	0.0462	0.1035
TL	0.9720	-0.2202
TW	0.0158	0.1238
HL	0.0123	0.1818
HW	0.0286	0.1637
HH	-0.0010	0.1013
FL	0.0299	0.0967
OD	0.0161	-0.0052
NE	0.0002	0.0720
SE	0.0032	0.0915
EE	0.0032	0.0565
EL	-0.0030	0.0209
IN	-0.0020	0.0209
IO	-0.0276	0.0740

Appendix III. Results of species delimitation using bPTP based on ML tree. Numbers above nodes/tips represent posterior delimitation probabilities from Bayesian reconstruction.



Species 11: *Hemidactylus* cf. *kushmorensis*

Species 9: *Hemidactylus parvimaculatus*

Species 10: *Hemidactylus* cf. *kushmorensis*

Species 1: *Hemidactylus chipkali* sp. nov.

Species 12: *Hemidactylus treutleri* (topotype)

Species 13: *Hemidactylus* cf. *treutleri*

Species 14: *Hemidactylus* cf. *treutleri*

Species 2: *Hemidactylus* cf. *murrayi*

Species 8: *Hemidactylus imbricatus*

Species 7: *Hemidactylus albofasciatus*

Species 5: *Hemidactylus reticulatus*

Species 6: *Hemidactylus satarensis*

Species 3: *Hemidactylus gracilis*

Species 4: *Hemidactylus* cf. *gleadowi*

Appendix IV. Results of bPTP showing support to each species.

bPTP results	Accession numbers	Species
Species 1 (support = 1.000)	KX044190	<i>Hemidactylus chipkali</i> sp. nov.
Species 2 (support = 0.909)	EU268407, GQ375294, GQ375293, EU268397, KU720667, KU720666, KU720676, HM595649, KU720674, KU720673, HM595659	<i>Hemidactylus</i> cf. <i>murrayi</i>
Species 3 (support = 1.000)	HM595660	<i>Hemidactylus gracilis</i>
Species 4 (support = 0.865)	KU720656, KU720657, KU720659, KU720660, KU720661, KU720662, KU720658	<i>Hemidactylus</i> cf. <i>gleadowi</i>
Species 5 (support = 0.689)	HM595670, HM595671, HM595669, EU268410	<i>Hemidactylus reticulatus</i>
Species 6 (support = 1.000)	HM595672	<i>Hemidactylus sataraensis</i>
Species 7 (support = 0.915)	HM595642, HM595643	<i>Hemidactylus albofasciatus</i>
Species 8 (support = 0.860)	EU268385, EU268386	<i>Hemidactylus imbricatus</i>
Species 9 (support = 0.754)	KU720640, KU720641, KU720644, KU720645, KU720647, KU720646, GQ375298, GQ375300, GQ375291, GQ375296, GQ375297, GQ375299, GQ375292, KU720637, DQ120271, DQ120272, HM595645, KU720638, GQ375290, DQ120273, KU720643, KU720642, KU720639	<i>Hemidactylus parvimaculatus</i>
Species 10 (support = 0.469)	KU720654, KU720653	<i>Hemidactylus</i> cf. <i>kushmorensis</i>
Species 11 (support = 0.539)	HM595647, HM595646, KU720650, KU720649, KU720652, KU720648, KU720651	<i>Hemidactylus</i> cf. <i>kushmorensis</i>
Species 12 (support = 1.000)	KU720681	<i>Hemidactylus treutleri</i> (topotype)
Species 13 (support = 0.594)	KU720679	<i>Hemidactylus</i> cf. <i>treutleri</i>
Species 14 (support = 0.425)	KU720677, KU720678	<i>Hemidactylus</i> cf. <i>treutleri</i>

A new gecko of the genus *Hemidactylus*

Appendix V (continued). Un-corrected pairwise sequence divergence between selected species of the genus *Hemidactylus* for the gene cytochrome *b*.

58	KU720667	0.17	0.17	0.16	0.17	0.17	0.16	0.00	0.02	0.20	0.16	0.16	0.16	0.00	0.00	0.16	0.16	0.17	0.16	0.16	0.18	0.18	0.17	0.15	0.16	0.03
59	KU720673	0.16	0.16	0.16	0.16	0.17	0.16	0.03	0.04	0.18	0.15	0.16	0.16	0.03	0.03	0.16	0.16	0.16	0.16	0.16	0.19	0.19	0.16	0.16	0.16	0.00
60	KU720674	0.16	0.16	0.16	0.16	0.17	0.16	0.03	0.04	0.18	0.15	0.16	0.16	0.03	0.03	0.16	0.16	0.16	0.16	0.16	0.19	0.19	0.16	0.16	0.16	0.00
61	KU720676	0.16	0.16	0.16	0.16	0.16	0.15	0.07	0.08	0.18	0.16	0.15	0.15	0.07	0.07	0.15	0.15	0.16	0.15	0.15	0.20	0.20	0.16	0.14	0.15	0.06
62	KU720677	0.17	0.17	0.16	0.14	0.15	0.17	0.11	0.13	0.17	0.15	0.16	0.16	0.11	0.11	0.16	0.16	0.17	0.16	0.16	0.18	0.18	0.17	0.16	0.16	0.12
63	KU720678	0.16	0.16	0.17	0.15	0.16	0.18	0.13	0.14	0.17	0.17	0.16	0.16	0.13	0.13	0.16	0.16	0.16	0.16	0.16	0.18	0.18	0.16	0.16	0.16	0.13
64	KU720679	0.17	0.17	0.17	0.15	0.15	0.15	0.11	0.13	0.16	0.17	0.17	0.17	0.11	0.11	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.15	0.16	0.10
65	KU720681	0.16	0.16	0.17	0.18	0.18	0.15	0.12	0.14	0.15	0.17	0.15	0.15	0.12	0.12	0.15	0.15	0.16	0.15	0.15	0.19	0.19	0.16	0.16	0.16	0.13
66	KX044190	0.22	0.22	0.21	0.17	0.18	0.17	0.13	0.14	0.20	0.20	0.22	0.22	0.13	0.13	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.11
58	KU720667	0.03	0.17	0.20	0.19	0.19	0.16	0.16	0.16	0.18	0.18	0.18	0.19	0.18	0.17	0.17	0.18	0.17	0.15	0.16	0.15	0.15	0.16	0.14	0.14	0.14
59	KU720673	0.00	0.17	0.18	0.17	0.17	0.16	0.16	0.15	0.18	0.18	0.18	0.18	0.17	0.17	0.18	0.17	0.17	0.16	0.16	0.16	0.15	0.16	0.14	0.14	0.14
60	KU720674	0.00	0.17	0.18	0.17	0.17	0.16	0.16	0.15	0.18	0.18	0.18	0.18	0.17	0.17	0.18	0.17	0.17	0.16	0.16	0.16	0.15	0.16	0.14	0.14	0.14
61	KU720676	0.06	0.16	0.18	0.17	0.17	0.17	0.15	0.15	0.17	0.17	0.17	0.18	0.17	0.16	0.16	0.18	0.16	0.14	0.15	0.14	0.14	0.15	0.15	0.15	0.13
62	KU720677	0.12	0.17	0.17	0.16	0.16	0.14	0.16	0.17	0.17	0.17	0.17	0.19	0.18	0.17	0.17	0.17	0.17	0.16	0.16	0.16	0.15	0.16	0.14	0.14	0.13
63	KU720678	0.13	0.18	0.17	0.16	0.16	0.13	0.16	0.16	0.17	0.17	0.17	0.18	0.18	0.16	0.17	0.16	0.16	0.16	0.17	0.16	0.16	0.16	0.16	0.16	0.14
64	KU720679	0.10	0.18	0.16	0.16	0.16	0.14	0.17	0.17	0.18	0.18	0.18	0.20	0.18	0.17	0.18	0.17	0.18	0.15	0.16	0.15	0.15	0.15	0.14	0.14	0.12
65	KU720681	0.13	0.17	0.16	0.16	0.16	0.16	0.15	0.16	0.15	0.15	0.15	0.17	0.17	0.16	0.15	0.16	0.16	0.16	0.16	0.16	0.15	0.17	0.16	0.16	0.14
66	KX044190	0.11	0.19	0.20	0.20	0.20	0.21	0.22	0.21	0.22	0.22	0.22	0.23	0.22	0.22	0.23	0.22	0.22	0.18	0.18	0.18	0.17	0.18	0.16	0.16	0.16
58	KU720667	0.13	0.13	0.12	0.13	0.14	0.13	0.02																		
59	KU720673	0.14	0.13	0.13	0.14	0.14	0.13	0.02	0.03																	
60	KU720674	0.14	0.13	0.13	0.14	0.14	0.13	0.02	0.03	0.00																
61	KU720676	0.13	0.12	0.14	0.14	0.13	0.13	0.06	0.07	0.06	0.06															
62	KU720677	0.13	0.13	0.13	0.14	0.13	0.14	0.13	0.11	0.12	0.12	0.14														
63	KU720678	0.14	0.14	0.14	0.15	0.14	0.15	0.14	0.13	0.13	0.13	0.15	0.03													
64	KU720679	0.12	0.13	0.12	0.13	0.11	0.13	0.11	0.11	0.10	0.10	0.12	0.04	0.05												
65	KU720681	0.14	0.13	0.13	0.14	0.14	0.14	0.14	0.12	0.13	0.13	0.13	0.10	0.09	0.10											
66	KX044190	0.17	0.16	0.16	0.16	0.16	0.16	0.11	0.13	0.11	0.11	0.14	0.15	0.17	0.14	0.16										